

Remarks

Claims 33-64 are in this case. Claims 1-32 have been cancelled. Claims 33-64 correspond essentially to claims 1-32. Since some of the claims include underlining and/or brackets, and to aid the Examiner, claims 1-32 were cancelled and replaced by claims 33-64.

In the Specification

Page 2 of the specification has been amended to delete the hyperlink.

In the Claims

The following are the main differences between claims 1-32 and claims 33-64. Other clerical corrections have been made.

Claim 33 (formerly claim 1)

Claim 33, line 1 "a candidate nucleotide sequence" has been replaced with -one or more candidate nucleotide sequences-

Claim 33, part (b) reads "assigning a score to each of a plurality of candidate nucleotide sequences, the score being obtained in a calculation using the probabilistic spectrum and at least one reference nucleotide sequence H;"

Claim 38 (formerly claim 6)

Claim 38, line 2 "based upon" has been changed to -obtained in a calculation using--

last line, "A" in the formula has been changed to E. This is supported by claim 33.

Claim 39 (formerly claim 7)

Claim 39, line 2 "based upon" has been changed to -obtained in a calculation using--

Claim 41 (formerly claim 9)

Claim 41, line 2 "based upon" has been changed to -obtained in a calculation using--

Claim 44 (formerly claim 12)

Claim 44, part (a) spelling of setting has been corrected

Claim 44, part (a) "a predetermined constant" has been changed to -a predetermined length-. This is supported by the disclosure on page 14, line 11.

Claim 44, part (c) reads

for each $j = l, l-1, \dots, m$, computing $R^u[\vec{y}, j]$ by initializing for each y

$R^u[\vec{y}, l] = 0$ and looping over

$$R^u[\vec{y}, j] = \max_{e=(\vec{y}, \vec{z}) \in E} \left\{ R^u[\vec{z}, j+1] + \omega(e) + L^{(j+1)}[z_{k-1}, h_{j+1}] \right\}$$

for all \vec{y}

Claim 56 (formerly claim 24)

Claim 56, lines 2 and 3 "a predetermined value" has been changed to -a predetermined score-. This is supported, *inter alia*, throughout the specification including at page 11, lines 13-15.

Claim 57 (formerly claim 25)

Claim 57, line 2 "based upon" has been changed to -obtained in a calculation using- last line, "A" in the formula has been changed to E. This is supported by claim 33.

Claim 63 (formerly claim 31)

Claim 63, line 2 of part (b) "based upon" has been changed to -obtained in a calculation using-

Claim 64 (formerly claim 32)

Claim 64, line 3 of part (b) "based upon" has been changed to --obtained in a calculation using--

The Examiner rejected claims 6 and 25 as not being enabled because of the use of the variable A in these claims. The replacement of A with E in these claims obviates the rejection.

The Examiner rejected claims 1-13, 15, 22, 24-29 and 31-32 under 35 USC 112, second paragraph.

Claim 33 includes the phrase "one or more candidate nucleotides sequences" in the preamble.

Claims 33, 63 and 64 include in part (b) that the score is obtained in a calculation using the probalistic spectrum..

Claims 38, 39, 41 and 57 include that the score is obtained in a calculation using the formula set out in the respective claim.

As stated above in Claim 44, part (a) "a predetermined constant" has been changed to --a predetermined length--. This is supported by the disclosure on page 14, line 11.

Formulae 14 and 15 are included in claim 44. Claim 44 depends from claim 43. This provides an antecedent basis for the formula

$$S''[\vec{y}, j] .$$

As stated above, in Claim 56, lines 2 and 3 "a predetermined value" has been changed to --a predetermined score--. This is supported *inter alia* throughout the specification including at page 11, lines 13-15.

Therefore, it is respectfully requested that the rejection be withdrawn.

There is a closed bracket in claim 43 and the spelling of setting was corrected in claim 44.

The Examiner rejected claims 1, 3-5, 31 and 32 as being anticipated by Sharaf (US Patent 5,873,052). Applicants respectfully traverse this rejection.

The Sharaf reference teaches comparing a known test sequence to a basis set of known sequences. The Sharaf reference nowhere mentions or even remotely hints at determining an unknown sequence of a biopolymer. The Examiner's assertion that the method of the Sharaf reference "allows for the identification of sequences" is incorrect. The Sharaf reference is therefore completely unrelated to the present invention which discloses a method for determining a sequence.

The Sharaf reference calculates a 'global matching probability' (Abstract) based upon a comparisons of the known sequences in the base set and the known sequence of the test sequence. The Sharaf reference nowhere compares each individual sequence in the basis set to the test sequence. Since the Sharaf reference only determines a single score, the Sharaf reference obviously nowhere mentions selecting a sequence having a maximum score.

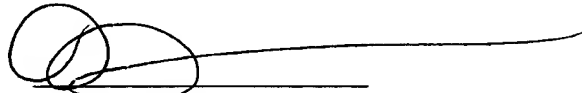
The DNA sequencer was used in the Sharaf reference to completely determine the complete sequence of the test sequence. This is different from a hybridization experiment which provides an indication of very short subsequences within the sequence. A hybridization experiment alone, unlike using a sequencer, does not unambiguously provide a sequence of a molecule. The present invention discloses a method for determining a sequence given the ambiguous results of a hybridization experiment and a reference sequence. The Sharaf reference nowhere mentions hybridization, and obviously does not deal with the problem of having to determine the sequence of molecule based upon the ambiguous results of a hybridization experiment.

Therefore, since Sharaf does not disclose each element of the invention claimed in

this application, Sharaf does not anticipate claims 1, 3-5, 31 and 32. It is respectfully requested that this rejection be withdrawn.

Accordingly, applicants submit that the present application is in condition for allowance and favorable consideration is respectfully requested.

Respectfully submitted,

A handwritten signature in black ink, consisting of a large, stylized 'J' and 'C' followed by a horizontal line extending to the right.

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In the Specification

Page 2, paragraph 5, please replace as follows:

National Center for Biotechnology Information, 2000, A database of single nucleotide polymorphisms, [<http://www.ncbi.nlm.nih.gov/SNP/>.]